

## GFAT-anglais

## SEQUENCE LISTING

<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE  
<120> GLUTAMINE:FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE (GFAT) COMPRISING AN INTERNAL PURIFICATION TAG, AND ITS USE FOR THE SCREENING OF COMPOUNDS  
<130> WOB 03 BP CNR GFAT  
<160> 19  
<170> PatentIn version 3.1  
<210> 1  
<211> 2046  
<212> DNA  
<213> Homo sapiens  
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cga gaa atc ctg gag acc cta atc aaa ggc ctt cag aga ctg gag tac		96
Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr		
20 25 30		
aga gga tat gat tct gct ggt gtg gga ttt gat gga ggc aat gat aaa		144
Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys		
35 40 45		
gat tgg gaa gcc aat gcc tgc aaa anc cag ctt att aag aag aaa gga		192
Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly		
50 55 60		
aaa gtt aag gca ctg gat gaa gaa gtt cac aag caa caa gat atg gat		240
Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp		
65 70 75 80		
ttg gat ata gaa ttt gat gta cac ctt gga ata gct cat acc cgt tgg		288
Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp		
85 90 95		
gca aca cat gga gaa ccc agt cct gtc aat agc cac ccc cag cgc tct		336
Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser		
100 105 110		
gat aaa aat aat gaa ttt atc gtt att cac aat gga atc atc acc aac		384

## GFAT-anglais

GFAT-anglais																
355	360				365											
ttg att ctt att gct tgt gga aca agt tac cat gct ggt gta gca aca	Leu Ile Leu Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Val Ala Thr															1152
370	375								380							
cgt caa gtt ctt gag gag ctg act gag ttg cct gtg atg gtg gaa cta	Arg Gln Val Leu Glu Glu Leu Thr Glu Leu Pro Val Met Val Glu Leu															1200
385	390							395								400
gca agt gac ttc ctg gac aga aac aca cca gtc ttt cga gat gat gtt	Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro Val Phe Arg Asp Asp Val															1248
405							410									415
tgc ttt ttc ctt agt caa tca ggt gag aca gca gat act ttg atg ggt	Cys Phe Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp Thr Leu Met Gly															1296
420							425									430
ctt cgt tac tgt aag gag aga gga gct tta act gtg ggg atc aca aac	Leu Arg Tyr Cys Lys Glu Arg Gly Ala Leu Thr Val Gly Ile Thr Asn															1344
435							440									445
aca gtt ggc agt tcc ata tca cgg gag aca gat tgt gga gtt cat att	Thr Val Gly Ser Ser Ile Ser Arg Gly Thr Asp Cys Gly Val His Ile															1392
450							455									
aat gct ggt cct gag att ggt gtg gcc agt aca aag gct tat acc agc	Asn Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser															1440
465							470									480
cag ttt gta tcc ctt gtg atg ttt gcc ctt atg atg tgt gat gat cgg	Gln Phe Val Ser Leu Val Met Phe Ala Leu Met Met Cys Asp Asp Arg															1488
485							490									495
atc tcc atg caa gaa aga cgc aaa gag atc atg ctt gga ttg aaa cgg	Ile Ser Met Gln Glu Arg Arg Lys Glu Ile Met Leu Gly Leu Lys Arg															1536
500							505									510
ctg cct gat ttg att aag gaa gta ctg agc atg gat gac gaa att cag	Leu Pro Asp Leu Ile Lys Glu Val Leu Ser Met Asp Asp Glu Ile Gln															1584
515							520									
aaa cta gca aca gaa ctt tat cat cag aag tca gtt ctg ata atg gga	Lys Leu Ala Thr Glu Leu Tyr His Gln Lys Ser Val Leu Ile Met Gly															1632
530							535									
cga ggc tat cat tat gct act tgt ctt gaa ggg gca ctg aaa atc aaa	Arg Gly Tyr His Tyr Ala Thr Cys Leu Glu Gly Ala Leu Lys Ile Lys															1680
545							550									560
gaa att act tat atg cac tct gaa ggc atc ctt gct ggt gaa ttg aaa	Glu Ile Thr Tyr Met His Ser Glu Gly Ile Leu Ala Gly Glu Leu Lys															1728
565							570									575
cat ggc cct ctg gct ttg gtg gat aaa ttg atg cct gtg atc atg atc	His Gly Pro Leu Ala Leu Val Asp Lys Leu Met Pro Val Ile Met Ile															1776
580							585									590
atc atg aga gat cac act tat gcc aag tgt cag aat gct ctt cag caa	Ile Met Arg Asp His Thr Tyr Ala Lys Cys Gln Asn Ala Leu Gln Gln															1824
595							600									605

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gtg gtt gct cgg cag ggg cgg cct gtg gta att tgt gat aag gag gat	1872
Val Val Ala Arg Gln Gly Arg Pro Val Val Ile Cys Asp Lys Glu Asp	
610 615 620	
act gag acc att aag aac aca aaa aga acg atc aag gtg ccc cac tca	1920
Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr Ile Lys Val Pro His Ser	
625 630 635 640	
gtg gac tgc ttg cag ggc att ctc agc gtg atc cct tta cag ttg ctg	1968
Val Asp Cys Leu Gln Gly Ile Leu Ser Val Ile Pro Leu Gln Leu Leu	
645 650 655	
gct ttc cac ctt gct gtg ctg aga ggc tat gat gtt gat ttc cca cgg	2016
Ala Phe His Leu Ala Val Leu Arg Gly Tyr Asp Val Asp Phe Pro Arg	
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aat ctt gcc aaa tct gtg act gta gag tga	2046
Asn Leu Ala Lys Ser Val Thr Val Glu	
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Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys	
35 40 45	
Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly	
50 55 60	
Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp	
65 70 75 80	
Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp	
85 90 95	
Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser	
100 105 110	
Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn	
115 120 125	
Tyr Lys Asp Leu Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu	
130 135 140	
Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr	
145 150 155 160	

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Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg  
 165 170 175  
 Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val  
 180 185 190  
 His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu  
 195 200 205  
 Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile  
 210 215 220  
 Leu Tyr Arg Thr Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu Ser Arg  
 225 230 235 240  
 Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala Val Glu  
 245 250 255  
 Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr Asn Arg  
 260 265 270  
 Val Ile Phe Leu Glu Asp Asp Asp Val Ala Ala Val Val Asp Gly Arg  
 275 280 285  
 Leu Ser Ile His Arg Ile Lys Arg Thr Ala Gly Asp His Pro Gly Arg  
 290 295 300  
 Ala Val Gln Thr Leu Gln Met Glu Leu Gln Gln Ile Met Lys Gly Asn  
 305 310 315 320  
 Phe Ser Ser Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Glu Ser Val  
 325 330 335  
 Val Asn Thr Met Arg Gly Arg Val Asn Phe Asp Asp Tyr Thr Val Asn  
 340 345 350  
 Leu Gly Gly Leu Lys Asp His Ile Lys Glu Ile Gln Arg Cys Arg Arg  
 355 360 365  
 Leu Ile Leu Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Val Ala Thr  
 370 375 380  
 Arg Gln Val Leu Glu Glu Leu Thr Glu Leu Pro Val Met Val Glu Leu  
 385 390 395 400  
 Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro Val Phe Arg Asp Asp Val  
 405 410 415  
 Cys Phe Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp Thr Leu Met Gly  
 420 425 430  
 Leu Arg Tyr Cys Lys Glu Arg Gly Ala Leu Thr Val Gly Ile Thr Asn  
 435 440 445  
 Thr Val Gly Ser Ser Ile Ser Arg Glu Thr Asp Cys Gly Val His Ile  
 450 455 460  
 Asn Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser  
 465 470 475 480  
 Gln Phe Val Ser Leu Val Met Phe Ala Leu Met Met Cys Asp Asp Arg

<b>485</b>	<b>GFAT-anglais</b>	<b>495</b>	
Ile Ser Met Gln Glu Arg Arg Lys Glu	Ile Met Leu Gly Leu Lys Arg		
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Leu Pro Asp Leu Ile Lys Glu Val	Leu Ser Met Asp Asp Glu Ile Gln		
515	520	525	
Lys Leu Ala Thr Glu Leu Tyr His Gln Lys Ser Val	Leu Ile Met Gly		
530	535	540	
Arg Gly Tyr His Tyr Ala Thr Cys Leu Glu Gly	Ala Leu Lys Ile Lys		
545	550	555	560
Glu Ile Thr Tyr Met His Ser Glu Gly	Ile Leu Ala Gly Glu Leu Lys		
565	570	575	
His Gly Pro Leu Ala Leu Val Asp Lys	Leu Met Pro Val Ile Met Ile		
580	585	590	
Ile Met Arg Asp His Thr Tyr Ala Lys Cys Gln Asn	Ala Leu Gln Gln		
595	600	605	
Val Val Ala Arg Gln Gly Arg Pro Val Val Ile Cys Asp Lys Glu Asp			
610	615	620	
Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr Ile Lys Val Pro His Ser			
625	630	635	640
Val Asp Cys Leu Gln Gly Ile Leu Ser Val Ile Pro Leu Gln Leu Leu			
645	650	655	
Ala Phe His Leu Ala Val Leu Arg Gly Tyr Asp Val Asp Phe Pro Arg			
660	665	670	
Asn Leu Ala Lys Ser Val Thr Val Glu			
675	680		

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Met Cys Gly Ile Phe Ala Tyr Met Asn Tyr Arg Val Pro Arg Thr Arg		
1 5 10 15		
aag gag atc ttc gaa acc ctc atc aag ggc ctg cag cgg ctg gag tac		96
Lys Glu Ile Phe Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr		
20 25 30		
aga ggc tac gac tcg gca ggt gtg gcg atc gat ggg aat aat cac gaa		144
Arg Gly Tyr Asp Ser Ala Gly Val Ala Ile Asp Gly Asn Asn His Glu		
35 40 45		
gtc aaa gaa aga cac att cag ctg gtc aag aaa agg ggg aaa gtc aag		192

GFAT-anglais															
Val	Lys	Glu	Arg	His	Ile	Gln	Leu	Val	Lys	Lys	Arg	Gly	Lys	Val	Lys
50									55			60			
gct	ctc	gat	gaa	gaa	ctt	tac	aaa	caa	gac	agc	atg	gac	tta	aaa	gtg
Ala	Leu	Asp	Glu	Glu	Leu	Tyr	Lys	Gln	Asp	Ser	Met	Asp	Leu	Lys	Val
65					70				75				80		
gag	ttt	gag	aca	cac	ttc	ggc	att	gcc	cac	acg	cgc	tgg	gcc	acc	cac
Glu	Phe	Glu	Thr	His	Phe	Gly	Ile	Ala	His	Thr	Arg	Trp	Ala	Thr	His
				85				90				95			
ggg	gtc	ccc	agt	gct	gtc	aac	agc	cac	cct	cag	cgc	tca	gac	aaa	ggc
Gly	Val	Pro	Ser	Ala	Val	Asn	Ser	His	Pro	Gln	Arg	Ser	Asp	Lys	Gly
				100				105				110			
aac	gaa	ttt	gtt	gtc	atc	cac	aat	ggg	atc	atc	aca	aat	tac	aaa	gat
Asn	Glu	Phe	Val	Val	Ile	His	Asn	Gly	Ile	Ile	Thr	Asn	Tyr	Lys	Asp
				115				120				125			
ctg	agg	aaa	ttt	ctg	gaa	agc	aaa	ggc	tac	gag	ttt	gag	tca	gaa	aca
Leu	Arg	Lys	Phe	Leu	Glu	Ser	Lys	Gly	Tyr	Gl	130	Phe	Gl	Ser	Glu
						135						140			
gat	aca	gag	acc	atc	gcc	aag	ctg	att	aaa	tat	gtg	ttc	gac	aac	aga
Asp	Thr	Glu	Thr	Ile	Ala	Lys	Leu	Ile	Lys	Tyr	Val	Phe	Asp	Asn	Arg
				145		150					155				160
gaa	act	gag	gac	att	acg	ttt	tca	acg	ttg	gtc	gag	aga	gtc	att	cag
Glu	Thr	Glu	Asp	Ile	Thr	Phe	Ser	Thr	Leu	Val	Glu	Arg	Val	Ile	Gln
					165				170				175		
cag	ttg	gaa	ggt	gca	ttc	gcg	ctg	gtt	ttc	aag	agt	gtc	cac	tac	cca
Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val	His	Tyr	Pro
					180				185				190		
gga	gaa	gcc	gtt	gcc	aca	cgg	aga	ggc	agc	ccc	ctg	ctc	atc	gga	gtc
Gly	Glu	Ala	Val	Ala	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu	Ile	Gly	Val
				195		200					205				
cgg	agc	aaa	tac	aag	ctc	tcc	aca	gaa	cag	atc	cct	atc	tta	tac	agg
Arg	Ser	Lys	Tyr	Lys	Leu	Ser	Thr	Glu	Gln	Ile	Pro	Ile	Leu	Tyr	Arg
				210		215					220				
acg	tgc	act	ctg	gag	aat	gtg	aag	aat	atc	tgt	aag	aca	cgg	atg	aag
Thr	Cys	Thr	Leu	Glu	Asn	Val	Lys	Asn	Ile	Cys	Lys	Thr	Arg	Met	Lys
				225		230				235				240	
agg	ctg	gac	agc	tcc	gcc	tgc	ctg	cat	gct	gtg	ggc	gac	aag	gcc	gtg
Arg	Leu	Asp	Ser	Ser	Ala	Cys	Leu	His	Ala	Val	Gly	Asp	Lys	Ala	Val
					245				250				255		
gaa	ttc	ttc	ttt	gct	tct	gat	gca	agc	gct	atc	ata	gag	cac	acc	aac
Glu	Phe	Phe	Ala	Ser	Asp	Ala	Ser	Ala	Ile	Ile	Glu	His	Thr	Asn	
					260				265				270		
cgg	gtc	atc	ttc	ctg	gag	gac	gat	gac	atc	gcc	gca	gtg	gct	gat	ggg
Arg	Val	Ile	Phe	Leu	Glu	Asp	Asp	Asp	Ile	Ala	Ala	Val	Ala	Asp	Gly
				275		280						285			
aaa	ctc	tcc	att	cac	cgg	gtc	aag	cgc	tcg	gcc	agt	gat	gac	cca	tct
Lys	Leu	Ser	Ile	His	Arg	Val	Lys	Arg	Ser	Ala	Ser	Asp	Asp	Pro	Ser

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cga	gcc	atc	cag	acc	ttg	cag	atg	gaa	ctg	cag	caa	atc	atg	aaa	ggt	960
Arg	Ala	Ile	Gln	Thr	Leu	Gln	Met	Glu	Leu	Gln	Gln	Ile	Met	Lys	Gly	
305					310				315						320	
aac	tcc	agt	gct	ttt	atg	cag	aag	gag	atc	ttc	gaa	cag	cca	gaa	tca	1008
Asn	Phe	Ser	Ala	Phe	Met	Gln	Lys	Glu	Ile	Phe	Glu	Gln	Pro	Glu	Ser	
					325				330					335		
gtt	tcc	aat	act	atg	aga	ggt	cgg	gtg	aat	ttt	gaa	acc	aac	aca	gtg	1056
Val	Phe	Asn	Thr	Met	Arg	Gly	Arg	Val	Asn	Phe	Glu	Thr	Asn	Thr	Val	
					340				345					350		
ctc	ctg	ggt	ggc	ttg	aag	gac	cac	ttg	aag	gag	att	cga	cga	tgc	cga	1104
Leu	Leu	Gly	Gly	Leu	Lys	Asp	His	Leu	Lys	Glu	Ile	Arg	Arg	Cys	Arg	
					355				360					365		
ccg	ctc	atc	gtg	att	ggc	tgt	gga	acc	agc	tac	cac	gct	gcc	gtg	gct	1152
Arg	Leu	Ile	Val	Ile	Gly	Cys	Gly	Thr	Ser	Tyr	His	Ala	Ala	Val	Ala	
					370				375					380		
acg	cgg	caa	gtt	ttg	gag	gaa	ctg	act	gag	ctt	cct	gtg	atg	gtt	gaa	1200
Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr	Glu	Leu	Pro	Val	Met	Val	Glu	
					385				390					400		
ctt	gct	agt	gat	ttt	ctg	gac	agg	aac	aca	cct	gtg	ttc	agg	gat	gac	1248
Leu	Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn	Thr	Pro	Val	Phe	Arg	Asp	Asp	
					405				410					415		
gtt	tgc	ttt	ttc	atc	agc	cag	tca	ggc	gag	acc	gct	gac	acc	ctc	ctg	1296
Val	Cys	Phe	Phe	Ile	Ser	Gln	Ser	Gly	Glu	Thr	Ala	Asp	Thr	Leu	Leu	
					420				425					430		
gcg	ctg	cgc	tac	tgt	aag	gac	cgc	ggc	gct	ctc	acc	gtg	ggc	gtc	acc	1344
Ala	Leu	Arg	Tyr	Cys	Lys	Asp	Arg	Gly	Ala	Leu	Thr	Val	Gly	Val	Thr	
					435				440					445		
aac	acc	gtg	ggc	agc	tcc	atc	tct	cgc	gag	acc	gac	tgc	ggc	gtc	cac	1392
Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	Glu	Thr	Asp	Cys	Gly	Val	His	
					450				455					460		
atc	aac	gca	ggg	ccg	gag	gtc	ggc	gtg	gcc	agc	acc	aag	gct	tat	acc	1440
Ile	Asn	Ala	Gly	Pro	Glu	Val	Gly	Val	Ala	Ser	Thr	Lys	Ala	Tyr	Thr	
					465				470					475		
agt	cag	tcc	atc	tct	ctg	gtg	atg	ttt	ggt	ttg	atg	atg	tct	gaa	gac	1488
Ser	Gln	Phe	Ile	Ser	Leu	Val	Met	Phe	Gly	Leu	Met	Met	Ser	Glu	Asp	
					485				490					495		
cga	att	tca	cta	caa	aac	agg	agg	caa	gag	atc	atc	cgt	ggc	ttg	aga	1536
Arg	Ile	Ser	Leu	Gln	Asn	Arg	Arg	Gln	Glu	Ile	Ile	Arg	Gly	Leu	Arg	
					500				505					510		
tct	tta	cct	gag	ctg	atc	aag	gaa	gtg	ctg	tct	ctg	gag	gag	aag	atc	1584
Ser	Leu	Pro	Glu	Leu	Ile	Lys	Glu	Val	Leu	Ser	Leu	Glu	Glu	Lys	Ile	
					515				520					525		
cac	gac	ttg	gcc	ctg	gag	ctc	tac	acg	cag	aga	tgc	ctg	ctg	gtg	atg	1632
His	Asp	Leu	Ala	Leu	Glu	Leu	Tyr	Thr	Gln	Arg	Ser	Leu	Leu	Val	Met	
					530				535					540		

GFAT-anglais

ggg	cgg	ggc	tac	aac	tat	gcc	acc	tgc	ctg	gaa	gga	gcc	ctg	aaa	att	1680
Gly	Arg	Gly	Tyr	Asn	Tyr	Ala	Thr	Cys	Leu	Glu	Gly	Ala	Leu	Lys	Ile	
545					550				555						560	
aaa	gag	ata	acc	tac	atg	cac	tca	gaa	ggc	atc	ctg	gct	ggg	gag	ctg	1728
Lys	Glu	Ile	Thr	Tyr	Met	His	Ser	Glu	Gly	Ile	Leu	Ala	Gly	Glu	Leu	
					565			570					575			
aag	cac	ggg	ccc	ctg	gca	ctg	att	gac	aag	cag	atg	ccc	gtc	atc	atg	1776
Lys	His	Gly	Pro	Leu	Ala	Leu	Ile	Asp	Lys	Gln	Met	Pro	Val	Ile	Met	
					580			585					590			
gtc	att	atg	aag	gat	cct	tgc	ttc	gcc	aaa	tgc	cag	aac	gcc	ctg	cag	1824
Val	Ile	Met	Lys	Asp	Pro	Cys	Phe	Ala	Lys	Cys	Gln	Asn	Ala	Leu	Gln	
					595		600				605					
caa	gtc	acg	gcc	cgc	cag	ggt	cgc	ccc	att	ata	ctg	tgc	tcc	aag	gac	1872
Gln	Val	Thr	Ala	Arg	Gln	Gly	Arg	Pro	Ile	Ile	Leu	Cys	Ser	Lys	Asp	
					610		615				620					
gat	act	gaa	agt	tcc	aag	ttt	gcg	tat	aag	aca	atc	gag	ctg	ccc	cac	1920
Asp	Thr	Glu	Ser	Ser	Lys	Phe	Ala	Tyr	Lys	Thr	Ile	Glu	Leu	Pro	His	
					625		630				635				640	
act	gtg	gac	tgc	ctc	cag	ggc	atc	ctg	agc	gtg	att	ccg	ctg	cag	ctg	1968
Thr	Val	Asp	Cys	Leu	Gln	Gly	Ile	Leu	Ser	Val	Ile	Pro	Leu	Gln	Leu	
					645		650				655					
ctg	tcc	ttc	cac	ctg	gct	gtt	ctc	cga	gga	tat	gac	gtt	gac	ttc	ccc	2016
Leu	Ser	Phe	His	Leu	Ala	Val	Leu	Arg	Gly	Tyr	Asp	Val	Asp	Phe	Pro	
					660		665				670					
aga	aat	ctg	gcc	aag	tct	gta	act	gtg	gaa	tga						2049
Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	Glu							
					675		680									

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Met	Cys	Gly	Ile	Phe	Ala	Tyr	Met	Asn	Tyr	Arg	Val	Pro	Arg	Thr	Arg	
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Lys	Glu	Ile	Phe	Glu	Thr	Leu	Ile	Lys	Gly	Leu	Gln	Arg	Leu	Glu	Tyr	
							20		25				30			
Arg	Gly	Tyr	Asp	Ser	Ala	Gly	Val	Ala	Ile	Asp	Gly	Asn	Asn	His	Glu	
							35		40				45			
Val	Lys	Glu	Arg	His	Ile	Gln	Leu	Val	Lys	Lys	Arg	Gly	Lys	Val	Lys	
							50		55				60			
Ala	Leu	Asp	Glu	Glu	Leu	Tyr	Lys	Gln	Asp	Ser	Met	Asp	Leu	Lys	Val	
							65		70				75			80
Glu	Phe	Glu	Thr	His	Phe	Gly	Ile	Ala	His	Thr	Arg	Trp	Ala	Thr	His	
							85		90				95			

GFAT-anglais

Gly Val Pro Ser Ala Val Asn Ser His Pro Gln Arg Ser Asp Lys Gly  
 100 105 110

Asn Glu Phe Val Val Ile His Asn Gly Ile Ile Thr Asn Tyr Lys Asp  
 115 120 125

Leu Arg Lys Phe Leu Glu Ser Lys Gly Tyr Glu Phe Ser Glu Thr  
 130 135 140

Asp Thr Glu Thr Ile Ala Lys Leu Ile Lys Tyr Val Phe Asp Asn Arg  
 145 150 155 160

Glu Thr Glu Asp Ile Thr Phe Ser Thr Leu Val Glu Arg Val Ile Gln  
 165 170 175

Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val His Tyr Pro  
 180 185 190

Gly Glu Ala Val Ala Thr Arg Arg Gly Ser Pro Leu Leu Ile Gly Val  
 195 200 205

Arg Ser Lys Tyr Lys Leu Ser Thr Glu Gln Ile Pro Ile Leu Tyr Arg  
 210 215 220

Thr Cys Thr Leu Glu Asn Val Lys Asn Ile Cys Lys Thr Arg Met Lys  
 225 230 235 240

Arg Leu Asp Ser Ser Ala Cys Leu His Ala Val Gly Asp Lys Ala Val  
 245 250 255

Glu Phe Phe Ala Ser Asp Ala Ser Ala Ile Ile Glu His Thr Asn  
 260 265 270

Arg Val Ile Phe Leu Glu Asp Asp Ile Ala Ala Val Ala Asp Gly  
 275 280 285

Lys Leu Ser Ile His Arg Val Lys Arg Ser Ala Ser Asp Asp Pro Ser  
 290 295 300

Arg Ala Ile Gln Thr Leu Gln Met Glu Leu Gln Gln Ile Met Lys Gly  
 305 310 315 320

Asn Phe Ser Ala Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Glu Ser  
 325 330 335

Val Phe Asn Thr Met Arg Gly Arg Val Asn Phe Glu Thr Asn Thr Val  
 340 345 350

Leu Leu Gly Gly Leu Lys Asp His Leu Lys Glu Ile Arg Arg Cys Arg  
 355 360 365

Arg Leu Ile Val Ile Gly Cys Gly Thr Ser Tyr His Ala Ala Val Ala  
 370 375 380

Thr Arg Gln Val Leu Glu Glu Leu Thr Glu Leu Pro Val Met Val Glu  
 385 390 395 400

Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro Val Phe Arg Asp Asp  
 405 410 415

Val Cys Phe Phe Ile Ser Gln Ser Gly Glu Thr Ala Asp Thr Leu Leu  
 420 425 430

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Ala Leu Arg Tyr Cys Lys Asp Arg Gly Ala Leu Thr Val Gly Val Thr  
435 440 445

Asn Thr Val Gly Ser Ser Ile Ser Arg Glu Thr Asp Cys Gly Val His  
450 455 460 465

Ile Asn Ala Gly Pro Glu Val Gly Val Ala Ser Thr Lys Ala Tyr Thr  
465 470 475 480

Ser Gln Phe Ile Ser Leu Val Met Phe Gly Leu Met Met Ser Glu Asp  
485 490 495

Arg Ile Ser Leu Gln Asn Arg Arg Gln Glu Ile Ile Arg Gly Leu Arg  
500 505 510

Ser Leu Pro Glu Leu Ile Lys Glu Val Leu Ser Leu Glu Glu Lys Ile  
515 520 525

His Asp Leu Ala Leu Glu Leu Tyr Thr Gln Arg Ser Leu Leu Val Met  
530 535 540

Gly Arg Gly Tyr Asn Tyr Ala Thr Cys Leu Glu Gly Ala Leu Lys Ile  
545 550 555 560

Lys Glu Ile Thr Tyr Met His Ser Glu Gly Ile Leu Ala Gly Glu Leu  
565 570 575

Lys His Gly Pro Leu Ala Leu Ile Asp Lys Gln Met Pro Val Ile Met  
580 585 590

Val Ile Met Lys Asp Pro Cys Phe Ala Lys Cys Gln Asn Ala Leu Gln  
595 600 605

Gln Val Thr Ala Arg Gln Gly Arg Pro Ile Ile Leu Cys Ser Lys Asp  
610 615 620

Asp Thr Glu Ser Ser Lys Phe Ala Tyr Lys Thr Ile Glu Leu Pro His  
625 630 635 640

Thr Val Asp Cys Leu Gln Gly Ile Leu Ser Val Ile Pro Leu Gln Leu  
645 650 655

Leu Ser Phe His Leu Ala Val Leu Arg Gly Tyr Asp Val Asp Phe Pro  
660 665 670

Arg Asn Leu Ala Lys Ser Val Thr Val Glu  
675 680

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<212> DNA  
<213> Homo sapiens

<220>  
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GFAT-anglais

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<222>	(170)..(170)																
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Met	Cys	Gly	Ile	Phe	Ala	Tyr	Leu	Asn	Tyr	His	Val	Pro	Arg	Thr	Arg		
1				5			10					15					
cga	gaa	atc	ctg	gag	acc	cta	atc	aaa	ggc	ctt	cag	aga	ctg	gag	tac	96	
Arg	Glu	Ile	Leu	Glu	Thr	Leu	Ile	Lys	Gly	Leu	Gln	Arg	Leu	Glu	Tyr		
				20			25					30					
aga	gga	tat	gat	tct	gct	ggt	gtg	gga	ttt	gat	gga	ggc	aat	gat	aaa	144	
Arg	Gly	Tyr	Asp	Ser	Ala	Gly	Val	Gly	Phe	Asp	Gly	Gly	Asn	Asp	Lys		
				35			40					45					
gat	tgg	gaa	gcc	aat	gcc	tgc	aaa	anc	cag	ctt	att	aag	aag	aaa	gga	192	
Asp	Trp	Glu	Ala	Asn	Ala	Cys	Lys	Xaa	Gln	Leu	Ile	Lys	Lys	Lys	Gly		
				50			55				60						
aaa	gtt	aag	gca	ctg	gat	gaa	gaa	gtt	cac	aag	caa	caa	gat	atg	gat	240	
Lys	Val	Lys	Ala	Leu	Asp	Glu	Glu	Val	His	Lys	Gln	Gln	Asp	Met	Asp		
				65			70				75						
ttg	gat	ata	gaa	ttt	gat	gta	cac	ctt	gga	ata	gct	cat	acc	cgt	tgg	288	
Leu	Asp	Ile	Glu	Phe	Asp	Val	His	Leu	Gly	Ile	Ala	His	Thr	Arg	Trp		
				85			90						95				
gca	aca	cat	gga	gaa	ccc	agt	cct	gtc	aat	agc	cac	ccc	cag	cgc	tct	336	
Ala	Thr	His	Gly	Glu	Pro	Ser	Pro	Val	Asn	Ser	His	Pro	Gln	Arg	Ser		
				100			105					110					
gat	aaa	aat	aat	gaa	ttt	atc	gtt	att	cac	aat	gga	atc	atc	acc	aac	384	
Asp	Lys	Asn	Asn	Glu	Phe	Ile	Val	Ile	His	Asn	Gly	Ile	Ile	Thr	Asn		
				115			120				125						
tac	aaa	gac	ttg	aaa	aag	ttt	ttg	gaa	agc	aaa	ggc	tat	gac	ttc	gaa	432	
Tyr	Lys	Asp	Leu	Lys	Lys	Phe	Leu	Glu	Ser	Lys	Gly	Tyr	Asp	Phe	Glu		
				130			135				140						
tct	gaa	aca	gac	aca	gag	aca	att	gcc	aag	ctc	gtt	aag	tat	atg	tat	480	
Ser	Glu	Thr	Asp	Thr	Glu	Thr	Ile	Ala	Lys	Leu	Val	Lys	Tyr	Met	Tyr		
				145			150				155				160		
gac	aat	cgg	gaa	agt	caa	gat	acc	agc	ttt	act	acc	ttg	gtg	gag	aga	528	
Asp	Asn	Arg	Glu	Ser	Gln	Asp	Thr	Ser	Phe	Thr	Thr	Leu	Val	Glu	Arg		
				165			170						175				
gtt	atc	caa	caa	ttg	gaa	ggt	gct	ttt	gca	ctt	gtg	ttt	aaa	agt	gtt	576	
Val	Ile	Gln	Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val		
				180			185					190					
cat	ttt	ccc	ggg	caa	gca	gtt	ggc	aca	agg	cga	ggt	agc	cct	ctg	ttg	624	
His	Phe	Pro	Gly	Gln	Ala	Val	Gly	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu		
				195			200					205					
att	ggt	gta	cgg	agt	gaa	cat	aaa	ctt	tct	act	gat	cac	att	cct	ata	672	
Ile	Gly	Val	Arg	Ser	Glu	His	Lys	Leu	Ser	Thr	Asp	His	Ile	Pro	Ile		
				210			215				220						

GFAT-anglais

ctc tac aga aca gct agg act cag att gga tca aaa ttc aca cgg tgg	720
Leu Tyr Arg Thr Ala Arg Thr Gln Ile Gly Ser Lys Phe Thr Arg Trp	
225 230 235 240	
gga tca cag gga gaa aga ggc aaa gac aag aaa gga agc tgc aat ctc	768
Gly Ser Gln Gly Glu Arg Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu	
245 250 255	
tct cgt gtg gac agc aca acc tgc ctt ttc ccg gtg gaa gaa aaa gca	816
Ser Arg Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala	
260 265 270	
gtg gag tat tac ttt gct tct gat gca agt gct gtc ata gaa cac acc	864
Val Glu Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr	
275 280 285	
aat cgc gtc atc ttt ctg gaa gat gat gat gtt gca gca gta gtg gat	912
Asn Arg Val Ile Phe Leu Glu Asp Asp Asp Val Ala Ala Val Val Asp	
290 295 300	
gga cgt ctt tct atc cat cga att aaa cga act gca gga gat cac ccc	960
Gly Arg Leu Ser Ile His Arg Ile Lys Arg Thr Ala Gly Asp His Pro	
305 310 315 320	
gga cga gct gtg caa aca ctc cag atg gaa ctc cag cag atc atg aag	1008
Gly Arg Ala Val Gln Thr Leu Gln Met Glu Leu Gln Gln Ile Met Lys	
325 330 335	
ggc aac ttc agt tca ttt atg cag aag gaa ata ttt gag cag cca gag	1056
Gly Asn Phe Ser Ser Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Glu	
340 345 350	
tct gtc gtg aac aca atg aga gga aga gtc aac ttt gat gac tat act	1104
Ser Val Val Asn Thr Met Arg Gly Arg Val Asn Phe Asp Asp Tyr Thr	
355 360 365	
gtg aat ttg ggt ggt ttg aag gat cac ata aag gag atc cag aga tgc	1152
Val Asn Leu Gly Gly Leu Lys Asp His Ile Lys Glu Ile Gln Arg Cys	
370 375 380	
cgg cgt ttg att ctt att gct tgt gga aca agt tac cat gct ggt gta	1200
Arg Arg Leu Ile Leu Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Val	
385 390 395 400	
gca aca cgt caa gtt ctt gag gag ctg act gag ttg cct gtg atg gtg	1248
Ala Thr Arg Gln Val Leu Glu Glu Leu Thr Glu Leu Pro Val Met Val	
405 410 415	
gaa cta gca agt gac ttc ctg gac aga aac aca cca gtc ttt cga gat	1296
Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro Val Phe Arg Asp	
420 425 430 435	
gat gtt tgc ttt ttc ctt agt caa tca ggt gag aca gca gat act ttg	1344
Asp Val Cys Phe Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp Thr Leu	
435 440 445	
atg ggt ctt cgt tac tgt aag gag aga gga gct tta act gtg ggg atc	1392
Met Gly Leu Arg Tyr Cys Lys Glu Arg Gly Ala Leu Thr Val Gly Ile	
450 455 460	

GFAT-anglais																	
aca	aac	aca	gtt	ggc	agt	tcc	ata	tca	cg <sup>g</sup>	gag	aca	gat	tgt	gga	gtt	1440	
Thr	Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	Glu	Thr	Asp	Cys	Gly	Val		
465			470						475						480		
cat	att	aat	gct	ggt	cct	gag	att	ggt	gtg	gcc	agt	aca	aag	gct	tat	1488	
His	Ile	Asn	Ala	Gly	Pro	Glu	Ile	Gly	Val	Ala	Ser	Thr	Lys	Ala	Tyr		
			485						490						495		
acc	agc	cag	ttt	gta	tcc	ctt	gtg	atg	ttt	gcc	ctt	atg	atg	tgt	gat	1536	
Thr	Ser	Gln	Phe	Val	Ser	Leu	Val	Met	Phe	Ala	Leu	Met	Met	Cys	Asp		
			500					505							510		
gat	cg <sup>g</sup>	atc	tcc	atg	caa	gaa	aga	cg <sup>c</sup>	aaa	gag	atc	atg	ctt	gga	ttg	1584	
Asp	Arg	Ile	Ser	Met	Gln	Glu	Arg	Arg	Lys	Glu	Ile	Met	Leu	Gly	Leu		
			515					520							525		
aaa	cg <sup>g</sup>	ctg	cct	gat	ttg	att	aag	gaa	gta	ctg	agc	atg	gat	gac	gaa	1632	
Lys	Arg	Leu	Pro	Asp	Leu	Ile	Lys	Glu	Val	Leu	Ser	Met	Asp	Asp	Glu		
			530			535					540						
att	cag	aaa	cta	gca	aca	gaa	ctt	tat	cat	cag	aag	tca	gtt	ctg	ata	1680	
Ile	Gln	Lys	Leu	Ala	Thr	Glu	Leu	Tyr	His	Gln	Lys	Ser	Val	Leu	Ile		
			545			550				555					560		
atg	gga	cga	ggc	tat	cat	tat	gct	act	tgt	ctt	gaa	ggg	gca	ctg	aaa	1728	
Met	Gly	Arg	Gly	Tyr	His	Tyr	Ala	Thr	Cys	Leu	Glu	Gly	Ala	Leu	Lys		
			565					570							575		
atc	aaa	gaa	att	act	tat	atg	cac	tct	gaa	ggc	atc	ctt	gct	ggt	gaa	1776	
Ile	Lys	Glu	Ile	Thr	Tyr	Met	His	Ser	Glu	Gly	Ile	Leu	Ala	Gly	Glu		
			580				585						590				
ttg	aaa	cat	ggc	cct	ctg	gct	ttg	gtg	gat	aaa	ttg	atg	cct	gtg	atc	1824	
Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Val	Asp	Lys	Leu	Met	Pro	Val	Ile		
			595				600					605					
atg	atc	atc	atc	atg	aga	gat	cac	act	tat	gcc	aag	tgt	cag	aat	gct	ctt	1872
Met	Ile	Ile	Met	Arg	Asp	His	Thr	Tyr	Ala	Lys	Cys	Gln	Asn	Ala	Leu		
			610			615				620							
cag	caa	gtg	gtt	gct	cg <sup>g</sup>	cag	ggg	cg <sup>c</sup>	cct	gtg	gta	att	tgt	gat	aag	1920	
Gln	Gln	Val	Val	Ala	Arg	Gln	Gly	Arg	Pro	Val	Val	Ile	Cys	Asp	Lys		
			625			630			635						640		
gag	gat	act	gag	acc	att	aag	aac	aca	aaa	aga	acg	atc	aag	gtg	ccc	1968	
Glu	Asp	Thr	Glu	Thr	Ile	Lys	Asn	Thr	Lys	Arg	Thr	Ile	Lys	Val	Pro		
			645					650						655			
cac	tca	gtg	gac	tgc	ttg	cag	ggc	att	ctc	agc	gtg	atc	cct	tta	cag	2016	
His	Ser	Val	Asp	Cys	Leu	Gln	Gly	Ile	Leu	Ser	Val	Ile	Pro	Leu	Gln		
			660			665						670					
ttg	ctg	gct	t <sup>t</sup> c	cac	ctt	gct	gtg	ctg	aga	ggc	tat	gat	gtt	gat	t <sup>t</sup> c	2064	
Leu	Leu	Ala	Phe	His	Leu	Ala	Val	Leu	Arg	Gly	Tyr	Asp	Val	Asp	Phe		
			675			680						685					
cca	cg <sup>g</sup>	aat	ctt	gcc	aaa	tct	gtg	act	gta	gag	tga					2100	
Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	Glu							
			690			695											

## GFAT-anglais

<210> 6  
<211> 699  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> (57);.(57)  
<223> 'Xaa' in position 57 represents Thr or Ile

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Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys  
35 40 45  
Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly  
50 55 60  
Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp  
65 70 75 80  
Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp  
85 90 95  
Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser  
100 105 110  
Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn  
115 120 125  
Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu  
130 135 140  
Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr  
145 150 155 160  
Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg  
165 170 175  
Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val  
180 185 190  
His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu  
195 200 205  
Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile  
210 215 220  
Leu Tyr Arg Thr Ala Arg Thr Gln Ile Gly Ser Lys Phe Thr Arg Trp  
225 230 235 240  
Gly Ser Gln Gly Glu Arg Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu  
245 250 255  
Ser Arg Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala  
260 265 270  
Val Glu Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr

GFAT-anglais

275	280	285
Asn Arg Val Ile Phe Leu Glu Asp Asp Asp Val Ala Ala Val Val Asp		
290 295 300		
Gly Arg Leu Ser Ile His Arg Ile Lys Arg Thr Ala Gly Asp His Pro		
305 310 315 320		
Gly Arg Ala Val Gln Thr Leu Gln Met Glu Leu Gln Gln Ile Met Lys		
325 330 335		
Gly Asn Phe Ser Ser Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Glu		
340 345 350		
Ser Val Val Asn Thr Met Arg Gly Arg Val Asn Phe Asp Asp Tyr Thr		
355 360 365		
Val Asn Leu Gly Gly Leu Lys Asp His Ile Lys Glu Ile Gln Arg Cys		
370 375 380		
Arg Arg Leu Ile Leu Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Val		
385 390 395 400		
Ala Thr Arg Gln Val Leu Glu Glu Leu Thr Glu Leu Pro Val Met Val		
405 410 415		
Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro Val Phe Arg Asp		
420 425 430		
Asp Val Cys Phe Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp Thr Leu		
435 440 445		
Met Gly Leu Arg Tyr Cys Lys Glu Arg Gly Ala Leu Thr Val Gly Ile		
450 455 460		
Thr Asn Thr Val Gly Ser Ser Ile Ser Arg Glu Thr Asp Cys Gly Val		
465 470 475 480		
His Ile Asn Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr		
485 490 495		
Thr Ser Gln Phe Val Ser Leu Val Met Phe Ala Leu Met Met Cys Asp		
500 505 510		
Asp Arg Ile Ser Met Gln Glu Arg Arg Lys Glu Ile Met Leu Gly Leu		
515 520 525		
Lys Arg Leu Pro Asp Leu Ile Lys Glu Val Leu Ser Met Asp Asp Glu		
530 535 540		
Ile Gln Lys Leu Ala Thr Glu Leu Tyr His Gln Lys Ser Val Leu Ile		
545 550 555 560		
Met Gly Arg Gly Tyr His Tyr Ala Thr Cys Leu Glu Gly Ala Leu Lys		
565 570 575		
Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly Ile Leu Ala Gly Glu		
580 585 590		
Leu Lys His Gly Pro Leu Ala Leu Val Asp Lys Leu Met Pro Val Ile		
595 600 605		

### GFAT-anglais

Met Ile Ile Met Arg Asp His Thr Tyr Ala Lys Cys Gln Asn Ala Leu  
 610 615 620  
 Gln Gln Val Val Ala Arg Gln Gly Arg Pro Val Val Ile Cys Asp Lys  
 625 630 635 640  
 Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr Ile Lys Val Pro  
 645 650 655  
 His Ser Val Asp Cys Leu Gln Gly Ile Leu Ser Val Ile Pro Leu Gln  
 660 665 670  
 Leu Leu Ala Phe His Leu Ala Val Leu Arg Gly Tyr Asp Val Asp Phe  
 675 680 685  
 Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu  
 690 695

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 <211> 2064  
 <212> DNA  
 <213> Artificial sequence

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<220>  
 <221> CDS  
 <222> (1)..(2064)  
 <223>

<220>  
 <221> misc\_feature  
 <222> (170)..(170)  
 <223> t or c

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 Met Cys Gly Ile Phe Ala Tyr Leu Asn Tyr His Val Pro Arg Thr Arg  
 1 5 10 15  
 cga gaa atc ctg gag acc cta atc aaa ggc ctt cag aga ctg gag tac 96  
 Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr  
 20 25 30  
 aga gga tat gat tct gct ggt gtg gga ttt gat gga ggc aat gat aaa 144  
 Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys  
 35 40 45  
 gat tgg gaa gcc aat gcc tgc aaa anc cag ctt att aag aag aaa gga 192  
 Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly  
 50 55 60  
 aaa gtt aag gca ctg gat gaa gaa gtt cac aag caa caa gat atg gat 240  
 Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp  
 65 70 75 80  
 ttg gat ata gaa ttt gat gta cac ctt gga ata gct cat acc cgt tgg 288

GFAT-anglais															
Leu	Asp	Ile	Glu	Phe	Asp	Val	His	Leu	Gly	Ile	Ala	His	Thr	Arg	Trp
85								90					95		
gca	aca	cat	gga	gaa	ccc	agt	cct	gtc	aat	agc	cac	ccc	cag	cgc	tct
Ala	Thr	His	Gly	Glu	Pro	Ser	Pro	Val	Asn	Ser	His	Pro	Gln	Arg	Ser
100								105					110		
gat	aaa	aat	aat	gaa	ttt	atc	gtt	att	cac	aat	gga	atc	atc	acc	aac
Asp	Lys	Asn	Asn	Glu	Phe	Ile	Val	Ile	His	Asn	Gly	Ile	Ile	Thr	Asn
115								120					125		
tac	aaa	gac	ttg	aaa	aag	ttt	ttg	gaa	agc	aaa	ggc	tat	gac	ttc	gaa
Tyr	Lys	Asp	Leu	Lys	Lys	Phe	Leu	Glu	Ser	Lys	Gly	Tyr	Asp	Phe	Glu
130								135					140		
tct	gaa	aca	gac	aca	gag	aca	att	gcc	aag	ctc	gtt	aag	tat	atg	tat
Ser	Glu	Thr	Asp	Thr	Glu	Thr	Ile	Ala	Lys	Leu	Val	Lys	Tyr	Met	Tyr
145								150					155		
gac	aat	cgg	gaa	agt	caa	gat	acc	agc	ttt	act	acc	ttg	gtg	gag	aga
Asp	Asn	Arg	Glu	Ser	Gln	Asp	Thr	Ser	Phe	Thr	Thr	Leu	Val	Glu	Arg
165								170					175		
gtt	atc	caa	caa	ttg	gaa	ggt	gct	ttt	gca	ctt	gtg	ttt	aaa	agt	gtt
Val	Ile	Gln	Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val
180								185					190		
cat	ttt	ccc	ggg	caa	gca	gtt	ggc	aca	agg	cga	ggt	agc	cct	ctg	ttg
His	Phe	Pro	Gly	Gln	Ala	Val	Gly	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu
195								200					205		
att	ggt	gta	cgg	agt	gaa	cat	aaa	ctt	tct	act	gat	cac	att	cct	ata
Ile	Gly	Val	Arg	Ser	Glu	His	Lys	Leu	Ser	Thr	Asp	His	Ile	Pro	Ile
210								215					220		
ctc	tac	aga	aca	ggc	aaa	gac	aag	aaa	gga	agc	tgc	aat	ctc	tct	cgt
Leu	Tyr	Arg	Thr	Gly	Lys	Asp	Lys	Lys	Gly	Ser	Cys	Asn	Leu	Ser	Arg
225								230					235		
gtg	gac	agc	aca	acc	tgc	ctt	ttc	ccg	gtg	gaa	gaa	aaa	gca	gtg	gag
Val	Asp	Ser	Thr	Thr	Cys	Leu	Phe	Pro	Val	Glu	Glu	Lys	Ala	Val	Glu
245								250					255		
tat	tac	ttt	gct	tct	gat	gca	agt	gct	gtc	ata	gaa	cac	acc	aat	cgc
Tyr	Tyr	Phe	Ala	Ser	Asp	Ala	Ser	Ala	Val	Ile	Glu	His	Thr	Asn	Arg
260								265					270		
gtc	atc	ttt	ctg	gaa	gat	gat	gat	gtt	gca	gca	gta	gtg	gat	gga	cgt
Val	Ile	Phe	Leu	Glu	Asp	Asp	Asp	Asp	Val	Ala	Ala	Val	Val	Asp	Gly
275								280					285		
ctt	tct	atc	cat	cga	att	aaa	cga	act	gca	gga	cat	cac	cat	cac	cat
Leu	Ser	Ile	His	Arg	Ile	Lys	Arg	Thr	Ala	Gly	His	His	His	His	His
290								295					300		
cac	gat	cac	ccc	gga	cga	gct	gtg	caa	aca	ctc	cag	atg	gaa	ctc	cag
His	Asp	His	Pro	Gly	Arg	Ala	Val	Gln	Thr	Leu	Gln	Met	Glu	Leu	Gln
305								310					315		
cag	atc	atc	atg	aag	ggc	aac	ttc	agt	tca	ttt	atg	cag	aag	gaa	ata
Gln	Ile	Met	Lys	Gly	Asn	Phe	Ser	Ser	Phe	Met	Gln	Lys	Glu	Ile	Phe
325								330					335		

GFAT-anglais																	
gag	cag	cca	gag	tct	gtc	gtg	aac	aca	atg	aga	gga	aga	gtc	aac	ttt	1056	
Glu	Gln	Pro	Glu	Ser	Val	Val	Asn	Thr	Met	Arg	Gly	Arg	Val	Asn	Phe		
340							345						350				
gat	gac	tat	act	gtg	aat	ttg	ggt	ttg	aag	gat	cac	ata	aag	gag		1104	
Asp	Asp	Tyr	Thr	Val	Asn	Leu	Gly	Gly	Leu	Lys	Asp	His	Ile	Lys	Glu		
355						360					365						
atc	cag	aga	tgc	cgg	cgt	ttg	att	ctt	att	gct	tgt	gga	aca	agt	tac		1152
Ile	Gln	Arg	Cys	Arg	Arg	Leu	Ile	Leu	Ile	Ala	Cys	Gly	Thr	Ser	Tyr		
370						375					380						
cat	gct	ggt	gta	gca	aca	cgt	caa	gtt	ctt	gag	gag	ctg	act	gag	ttg		1200
His	Ala	Gly	Val	Ala	Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr	Glu	Leu		
385						390				395				400			
cct	gtg	atg	gtg	gaa	cta	gca	agt	gac	ttc	ctg	gac	aga	aac	aca	cca		1248
Pro	Val	Met	Val	Glu	Leu	Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn	Thr	Pro		
				405					410				415				
gtc	ttt	cga	gat	gat	gtt	tgc	ttt	ttc	ctt	agt	caa	tca	ggt	gag	aca		1296
Val	Phe	Arg	Asp	Asp	Val	Cys	Phe	Phe	Leu	Ser	Gln	Ser	Gly	Glu	Thr		
				420				425					430				
gca	gat	act	ttg	atg	ggt	ctt	cgt	tac	tgt	aag	gag	aga	gga	gct	tta		1344
Ala	Asp	Thr	Leu	Met	Gly	Leu	Arg	Tyr	Cys	Lys	Glu	Arg	Gly	Ala	Leu		
				435				440				445					
act	gtg	ggg	atc	aca	aac	aca	gtt	ggc	agt	tcc	ata	tca	cgg	gag	aca		1392
Thr	Val	Gly	Ile	Thr	Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	Glu	Thr		
				450				455			460						
gat	tgt	gga	gtt	cat	att	aat	gct	ggt	cct	gag	att	ggt	gtg	gcc	agt		1440
Asp	Cys	Gly	Val	His	Ile	Asn	Ala	Gly	Pro	Glu	Ile	Gly	Val	Ala	Ser		
				465				470			475			480			
aca	aag	gct	tat	acc	agc	cag	ttt	gtt	tcc	ctt	gtg	atg	ttt	gcc	ctt		1488
Thr	Lys	Ala	Tyr	Thr	Ser	Gln	Phe	Val	Ser	Leu	Val	Met	Phe	Ala	Leu		
				485				490					495				
atg	atg	tgt	gat	gat	cgg	atc	tcc	atg	caa	gaa	aga	cgc	aaa	gag	atc		1536
Met	Met	Cys	Asp	Asp	Arg	Ile	Ser	Met	Gln	Glu	Arg	Arg	Lys	Glu	Ile		
				500				505					510				
atg	ctt	gga	ttg	aaa	cgg	ctg	cct	gat	ttg	att	aag	gaa	gta	ctg	agc		1584
Met	Leu	Gly	Leu	Lys	Arg	Leu	Pro	Asp	Leu	Ile	Lys	Glu	Val	Leu	Ser		
				515				520			525						
atg	gat	gac	gaa	att	cag	aaa	cta	gca	aca	gaa	ctt	tat	cat	cag	aag		1632
Met	Asp	Asp	Glu	Ile	Gln	Lys	Leu	Ala	Thr	Glu	Leu	Tyr	His	Gln	Lys		
				530				535			540						
tca	gtt	ctg	ata	atg	gga	cga	ggc	tat	cat	tat	gct	act	tgt	ctt	gaa		1680
Ser	Val	Leu	Ile	Met	Gly	Arg	Gly	Tyr	His	Tyr	Ala	Thr	Cys	Leu	Glu		
				545				550			555			560			
ggg	gca	ctg	aaa	atc	aaa	gaa	att	act	tat	atg	cac	tct	gaa	ggc	atc		1728
Gly	Ala	Leu	Lys	Ile	Lys	Glu	Ile	Thr	Tyr	Met	His	Ser	Glu	Gly	Ile		
				565				570			575						
ctt	gct	ggt	gaa	ttg	aaa	cat	ggc	cct	ctg	gct	ttg	gtg	gat	aaa	ttg		1776

GFAT-anglais

Leu	Ala	Gly	Glu	Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Val	Asp	Lys	Leu	
580								585								590
atg	cct	gtg	atc	atc	atc	atc	atg	aga	gat	cac	act	tat	gcc	aag	tgt	1824
Met	Pro	Val	Ile	Met	Ile	Ile	Met	Arg	Asp	His	Thr	Tyr	Ala	Lys	Cys	
595							600								605	
cag	aat	gct	ctt	cag	caa	gtg	gtt	gct	cgg	cag	ggg	cgg	cct	gtg	gta	1872
Gln	Asn	Ala	Leu	Gln	Gln	Val	Val	Ala	Arg	Gln	Gly	Arg	Pro	Val	Val	
610						615				620						
att	tgt	gat	aag	gag	gat	act	gag	acc	att	aag	aac	aca	aaa	aga	acg	1920
Ile	Cys	Asp	Lys	Glu	Asp	Thr	Glu	Thr	Ile	Lys	Asn	Thr	Lys	Arg	Thr	
625				630				635							640	
atc	aag	gtg	ccc	cac	tca	gtg	gac	tgc	ttg	cag	ggc	att	ctc	agc	gtg	1968
Ile	Lys	Val	Pro	His	Ser	Val	Asp	Cys	Leu	Gln	Gly	Ile	Leu	Ser	Val	
								645	650					655		
atc	cct	tta	cag	ttg	ctg	gct	ttc	cac	ctt	gct	gtg	ctg	aga	ggc	tat	2016
Ile	Pro	Leu	Gln	Leu	Leu	Ala	Phe	His	Leu	Ala	Val	Leu	Arg	Gly	Tyr	
								660	665					670		
gat	gtt	gat	ttc	cca	cgg	aat	ctt	gcc	aaa	tct	gtg	act	gta	gag	tga	2064
Asp	Val	Asp	Phe	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	Glu		
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<211> 687

<212> PRT

<213> Artificial sequence

<220>

<221> misc\_feature

<222> (57);.(57)

<223> 'Xaa' in position 57 represents Thr or Ile

<220>

<223> modified GFAT1 by an internal purification tag

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Arg	Glu	Ile	Leu	Glu	Thr	Leu	Ile	Lys	Gly	Leu	Gln	Arg	Leu	Glu	Tyr
20							25					30			

Arg	Gly	Tyr	Asp	Ser	Ala	Gly	Val	Gly	Phe	Asp	Gly	Gly	Asn	Asp	Lys
35							40					45			

Asp	Trp	Glu	Ala	Asn	Ala	Cys	Lys	Xaa	Gln	Leu	Ile	Lys	Lys	Gly	
50						55				60					

Lys	Val	Lys	Ala	Leu	Asp	Glu	Glu	Val	His	Lys	Gln	Gln	Asp	Met	Asp
65					70				75					80	

Leu	Asp	Ile	Glu	Phe	Asp	Val	His	Leu	Gly	Ile	Ala	His	Thr	Arg	Trp
85								90					95		

Ala	Thr	His	Gly	Glu	Pro	Ser	Pro	Val	Asn	Ser	His	Pro	Gln	Arg	Ser
100								105					110		

GFAT-anglais

Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn  
 115 120 125

Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu  
 130 135 140

Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr  
 145 150 155 160

Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg  
 165 170 175

Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val  
 180 185 190

His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu  
 195 200 205

Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile  
 210 215 220

Leu Tyr Arg Thr Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu Ser Arg  
 225 230 235 240

Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala Val Glu  
 245 250 255

Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr Asn Arg  
 260 265 270

Val Ile Phe Leu Glu Asp Asp Asp Val Ala Ala Val Val Asp Gly Arg  
 275 280 285

Leu Ser Ile His Arg Ile Lys Arg Thr Ala Gly His His His His His  
 290 295 300

His Asp His Pro Gly Arg Ala Val Gln Thr Leu Gln Met Glu Leu Gln  
 305 310 315 320

Gln Ile Met Lys Gly Asn Phe Ser Ser Phe Met Gln Lys Glu Ile Phe  
 325 330 335

Glu Gln Pro Glu Ser Val Val Asn Thr Met Arg Gly Arg Val Asn Phe  
 340 345 350

Asp Asp Tyr Thr Val Asn Leu Gly Gly Leu Lys Asp His Ile Lys Glu  
 355 360 365

Ile Gln Arg Cys Arg Arg Leu Ile Leu Ile Ala Cys Gly Thr Ser Tyr  
 370 375 380

His Ala Gly Val Ala Thr Arg Gln Val Leu Glu Glu Leu Thr Glu Leu  
 385 390 395 400

Pro Val Met Val Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro  
 405 410 415

Val Phe Arg Asp Asp Val Cys Phe Phe Leu Ser Gln Ser Gly Glu Thr  
 420 425 430

Ala Asp Thr Leu Met Gly Leu Arg Tyr Cys Lys Glu Arg Gly Ala Leu

GFAT-anglais

435	440	445
Thr Val Gly Ile Thr Asn Thr Val Gly Ser Ser Ile Ser Arg Glu Thr		
450	455	460
Asp Cys Gly Val His Ile Asn Ala Gly Pro Glu Ile Gly Val Ala Ser		
465	470	475
Thr Lys Ala Tyr Thr Ser Gln Phe Val Ser Leu Val Met Phe Ala Leu		
485	490	495
Met Met Cys Asp Asp Arg Ile Ser Met Gln Glu Arg Arg Lys Glu Ile		
500	505	510
Met Leu Gly Leu Lys Arg Leu Pro Asp Leu Ile Lys Glu Val Leu Ser		
515	520	525
Met Asp Asp Glu Ile Gln Lys Leu Ala Thr Glu Leu Tyr His Gln Lys		
530	535	540
Ser Val Leu Ile Met Gly Arg Gly Tyr His Tyr Ala Thr Cys Leu Glu		
545	550	555
Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly Ile		
565	570	575
Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Val Asp Lys Leu		
580	585	590
Met Pro Val Ile Met Ile Ile Met Arg Asp His Thr Tyr Ala Lys Cys		
595	600	605
Gln Asn Ala Leu Gln Gln Val Val Ala Arg Gln Gly Arg Pro Val Val		
610	615	620
Ile Cys Asp Lys Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr		
625	630	635
Ile Lys Val Pro His Ser Val Asp Cys Leu Gln Gly Ile Leu Ser Val		
645	650	655
Ile Pro Leu Gln Leu Leu Ala Phe His Leu Ala Val Leu Arg Gly Tyr		
660	665	670
Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu		
675	680	685

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<211> 2067  
<212> DNA  
<213> Artificial sequence

<220>  
<223> modified GFAT2 by an internal purification tag

<220>  
<221> CDS  
<222> (1)..(2067)  
<223>

<400> 9

GFAT-anglais																
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1				5					10					15		
aag	gag	atc	ttc	gaa	acc	ctc	atc	aag	ggc	ctg	cag	cgg	ctg	gag	tac	96
Lys	Glu	Ile	Phe	Glu	Thr	Leu	Ile	Lys	Gly	Leu	Gln	Arg	Leu	Glu	Tyr	
				20				25					30			
aga	ggc	tac	gac	tcg	gca	ggt	gtg	gcf	atc	gat	ggg	aat	aat	cac	gaa	144
Arg	Gly	Tyr	Asp	Ser	Ala	Gly	Val	Ala	Ile	Asp	Gly	Asn	Asn	His	Glu	
				35				40				45				
gtc	aaa	gaa	aga	cac	att	cag	ctg	gtc	aag	aaa	agg	ggg	aaa	gtc	aag	192
Val	Lys	Glu	Arg	His	Ile	Gln	Leu	Val	Lys	Lys	Arg	Gly	Lys	Val	Lys	
				50			55				60					
gct	ctc	gat	gaa	gaa	ctt	tac	aaa	caa	gac	agc	atg	gac	tta	aaa	gtg	240
Ala	Leu	Asp	Glu	Glu	Leu	Tyr	Lys	Gln	Asp	Ser	Met	Asp	Leu	Lys	Val	
				65			70			75			80			
gag	ttt	gag	aca	cac	ttc	ggc	att	gcc	cac	acg	cgc	tgg	gcc	acc	cac	288
Glu	Phe	Glu	Thr	His	Phe	Gly	Ile	Ala	His	Thr	Arg	Trp	Ala	Thr	His	
				85			90						95			
ggg	gtc	ccc	agt	gct	gtc	aac	agc	cac	cct	cag	cgc	tca	gac	aaa	ggc	336
Gly	Val	Pro	Ser	Ala	Val	Asn	Ser	His	Pro	Gln	Arg	Ser	Asp	Lys	Gly	
				100			105						110			
aac	gaa	ttt	gtt	gtc	atc	cac	aat	ggg	atc	atc	aca	aat	tac	aaa	gat	384
Asn	Glu	Phe	Val	Val	Ile	His	Asn	Gly	Ile	Ile	Thr	Asn	Tyr	Lys	Asp	
				115			120					125				
ctg	agg	aaa	ttt	ctg	gaa	agc	aaa	ggc	tac	gag	ttt	gag	tca	gaa	aca	432
Leu	Arg	Lys	Phe	Leu	Glu	Ser	Lys	Gly	Tyr	Glu	Phe	Glu	Ser	Glu	Thr	
				130			135				140					
gat	aca	gag	acc	atc	gcc	aag	ctg	att	aaa	tat	gtg	ttc	gac	aac	aga	480
Asp	Thr	Glu	Thr	Ile	Ala	Lys	Leu	Ile	Lys	Tyr	Val	Phe	Asp	Asn	Arg	
				145			150			155			160			
gaa	act	gag	gac	att	acg	ttt	tca	acg	ttg	gtc	gag	aga	gtc	att	cag	528
Glu	Thr	Glu	Asp	Ile	Thr	Phe	Ser	Thr	Leu	Val	Glu	Arg	Val	Ile	Gln	
				165			170						175			
cag	ttg	gaa	ggt	gca	ttc	gcf	ctg	gtt	ttc	aag	agt	gtc	cac	tac	cca	576
Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val	His	Tyr	Pro	
				180			185						190			
gga	gaa	gcc	gtt	gcc	aca	cgf	aga	ggc	agc	ccc	ctg	ctc	atc	gga	gtc	624
Gly	Glu	Ala	Val	Ala	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu	Ile	Gly	Val	
				195			200					205				
cgf	agc	aaa	tac	aag	ctc	tcc	aca	gaa	cag	atc	cct	atc	tta	tac	agg	672
Arg	Ser	Lys	Tyr	Lys	Leu	Ser	Thr	Glu	Gln	Ile	Pro	Ile	Leu	Tyr	Arg	
				210			215			220						
acg	tgc	act	ctg	gag	aat	gtg	aag	aat	atc	tgt	aag	aca	cgg	atg	aag	720
Thr	Cys	Thr	Leu	Glu	Asn	Val	Lys	Asn	Ile	Cys	Lys	Thr	Arg	Met	Lys	
				225			230			235				240		
agg	ctg	gac	agc	tcc	gcc	tgc	ctg	cat	gct	gtg	ggc	gac	aag	gcc	gtg	768
Arg	Leu	Asp	Ser	Ser	Ala	Cys	Leu	His	Ala	Val	Gly	Asp	Lys	Ala	Val	
				245			250						255			

GFAT-anglais

gaa ttc ttc ttt gct tct gat gca agc gct atc ata gag cac acc aac	816
Glu Phe Phe Phe Ala Ser Asp Ala Ser Ala Ile Ile Glu His Thr Asn	
260 265 270	
cgg gtc atc ttc ctg gag gac gat gac atc gcc gca gtg gct gat ggg	864
Arg Val Ile Phe Leu Glu Asp Asp Asp Ile Ala Ala Val Ala Asp Gly	
275 280 285	
aaa ctc tcc att cac cgg gtc aag cgc tcg gcc agt cat cac cat cac	912
Lys Leu Ser Ile His Arg Val Lys Arg Ser Ala Ser His His His His	
290 295 300	
cat cac gat gac cca tct cga gcc atc cag acc ttg cag atg gaa ctg	960
His His Asp Asp Pro Ser Arg Ala Ile Gln Thr Leu Gln Met Glu Leu	
305 310 315 320	
cag caa atc atg aaa ggt aac ttc agt gcg ttt atg cag aag gag atc	1008
Gln Gln Ile Met Lys Gly Asn Phe Ser Ala Phe Met Gln Lys Glu Ile	
325 330 335	
ttc gaa cag cca gaa tca gtt ttc aat act atg aga ggt cgg gtg aat	1056
Phe Glu Gln Pro Glu Ser Val Phe Asn Thr Met Arg Gly Arg Val Asn	
340 345 350	
ttt gaa acc aac aca gtg ctc ctg ggt ggc ttg aag gac cac ttg aag	1104
Phe Glu Thr Asn Thr Val Leu Leu Gly Gly Leu Lys Asp His Leu Lys	
355 360 365	
gag att cga cga tgc cga cgg ctc atc gtg att ggc tgt gga acc agc	1152
Glu Ile Arg Arg Cys Arg Arg Leu Ile Val Ile Gly Cys Gly Thr Ser	
370 375 380	
tac cac gct gcc gtg gct acg cgg caa gtt ttg gag gaa ctg act gag	1200
Tyr His Ala Ala Val Ala Thr Arg Gln Val Leu Glu Glu Leu Thr Glu	
385 390 395 400	
ctt cct gtg atg gtt gaa ctt gct agt gat ttt ctg gac agg aac aca	1248
Leu Pro Val Met Val Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr	
405 410 415	
cct gtg ttc agg gat gac gtt tgc ttt ttc atc agc cag tca ggc gag	1296
Pro Val Phe Arg Asp Asp Val Cys Phe Phe Ile Ser Gln Ser Gly Glu	
420 425 430	
acc gcg gac acc ctc ctg gcg ctg cgc tac tgt aag gac cgc ggc gct	1344
Thr Ala Asp Thr Leu Leu Ala Leu Arg Tyr Cys Lys Asp Arg Gly Ala	
435 440 445	
ctc acc gtg ggc gtc acc aac acc gtg ggc agc tcc atc tct cgc gag	1392
Leu Thr Val Gly Val Thr Asn Thr Val Gly Ser Ser Ile Ser Arg Glu	
450 455 460	
acc gac tgc ggc gtc cac atc aac gca ggg ccg gag gtc ggc gtg gcc	1440
Thr Asp Cys Gly Val His Ile Asn Ala Gly Pro Glu Val Gly Val Ala	
465 470 475 480	
agc acc aag gct tat acc agt cag ttc atc tct ctg gtg atg ttt ggt	1488
Ser Thr Lys Ala Tyr Thr Ser Gln Phe Ile Ser Leu Val Met Phe Gly	
485 490 495	
ttg atg atg tct gaa gac cga att tca cta caa aac agg agg caa gag	1536
Leu Met Met Ser Glu Asp Arg Ile Ser Leu Gln Asn Arg Arg Gln Glu	

GFAT-anglais

500	505	510	
atc atc cgt ggc ttg aga tct tta cct gag ctg atc aag gaa gtg ctg Ile Ile Arg Gly Leu Arg Ser Leu Pro Glu Leu Ile Lys Glu Val Leu 515 520 525			1584
tct ctg gag gag aag atc cac gac ttg gcc ctg gag ctc tac acg cag Ser Leu Glu Glu Lys Ile His Asp Leu Ala Leu Glu Leu Tyr Thr Gln 530 535 540			1632
aga tcg ctg ctg gtg atg ggg cgg ggc tac aac tat gcc acc tgc ctg Arg Ser Leu Leu Val Met Gly Arg Gly Tyr Asn Tyr Ala Thr Cys Leu 545 550 555 560			1680
gaa gga gcc ctg aaa att aaa gag ata acc tac atg cac tca gaa ggc Glu Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly 565 570 575			1728
atc ctg gct ggg gag ctg aag cac ggg ccc ctg gca ctg att gac aag Ile Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp Lys 580 585 590			1776
cag atg ccc gtc atc atg gtc att atg aag gat cct tgc ttc gcc aaa Gln Met Pro Val Ile Met Val Ile Met Lys Asp Pro Cys Phe Ala Lys 595 600 605			1824
tgc cag aac gcc ctg cag caa gtc acg gcc cgc cag ggt cgc ccc att Cys Gln Asn Ala Leu Gln Gln Val Thr Ala Arg Gln Gly Arg Pro Ile 610 615 620			1872
ata ctg tgc tcc aag gac gat act gaa agt tcc aag ttt gcg tat aag Ile Leu Cys Ser Lys Asp Asp Thr Glu Ser Ser Lys Phe Ala Tyr Lys 625 630 635 640			1920
aca atc gag ctg ccc cac act gtg gac tgc ctc cag ggc atc ctg agc Thr Ile Glu Leu Pro His Thr Val Asp Cys Leu Gln Gly Ile Leu Ser 645 650 655			1968
gtg att ccg ctg cag ctg ctg tcc ttc cac ctg gct gtt ctc cga gga Val Ile Pro Leu Gln Leu Leu Ser Phe His Leu Ala Val Leu Arg Gly 660 665 670			2016
tat gac gtt gac ttc ccc aga aat ctg gcc aag tct gta act gtg gaa Tyr Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu 675 680 685			2064
tga			2067

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<213> Artificial sequence

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Lys Glu Ile Phe Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr  
Page 25

GFAT-anglais

20	25	30
Arg Gly Tyr Asp Ser Ala Gly Val Ala Ile Asp Gly Asn Asn His Glu		
35 35 40 45		
Val Lys Glu Arg His Ile Gln Leu Val Lys Lys Arg Gly Lys Val Lys		
50 55 60		
Ala Leu Asp Glu Glu Leu Tyr Lys Gln Asp Ser Met Asp Leu Lys Val		
65 70 75 80		
Glu Phe Glu Thr His Phe Gly Ile Ala His Thr Arg Trp Ala Thr His		
85 90 95		
Gly Val Pro Ser Ala Val Asn Ser His Pro Gln Arg Ser Asp Lys Gly		
100 105 110		
Asn Glu Phe Val Val Ile His Asn Gly Ile Ile Thr Asn Tyr Lys Asp		
115 120 125		
Leu Arg Lys Phe Leu Glu Ser Lys Gly Tyr Glu Phe Glu Ser Glu Thr		
130 135 140		
Asp Thr Glu Thr Ile Ala Lys Leu Ile Lys Tyr Val Phe Asp Asn Arg		
145 150 155 160		
Glu Thr Glu Asp Ile Thr Phe Ser Thr Leu Val Glu Arg Val Ile Gln		
165 170 175		
Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val His Tyr Pro		
180 185 190		
Gly Glu Ala Val Ala Thr Arg Arg Gly Ser Pro Leu Leu Ile Gly Val		
195 200 205		
Arg Ser Lys Tyr Lys Leu Ser Thr Glu Gln Ile Pro Ile Leu Tyr Arg		
210 215 220		
Thr Cys Thr Leu Glu Asn Val Lys Asn Ile Cys Lys Thr Arg Met Lys		
225 230 235 240		
Arg Leu Asp Ser Ser Ala Cys Leu His Ala Val Gly Asp Lys Ala Val		
245 250 255		
Glu Phe Phe Phe Ala Ser Asp Ala Ser Ala Ile Ile Glu His Thr Asn		
260 265 270		
Arg Val Ile Phe Leu Glu Asp Asp Asp Ile Ala Ala Val Ala Asp Gly		
275 280 285		
Lys Leu Ser Ile His Arg Val Lys Arg Ser Ala Ser His His His His		
290 295 300		
His His Asp Asp Pro Ser Arg Ala Ile Gln Thr Leu Gln Met Glu Leu		
305 310 315 320		
Gln Gln Ile Met Lys Gly Asn Phe Ser Ala Phe Met Gln Lys Glu Ile		
325 330 335		
Phe Glu Gln Pro Glu Ser Val Phe Asn Thr Met Arg Gly Arg Val Asn		
340 345 350		
Phe Glu Thr Asn Thr Val Leu Leu Gly Gly Leu Lys Asp His Leu Lys		

		<b>GFAT-anglais</b>
355	360	365
Glu Ile Arg Arg Cys Arg Arg	Leu Ile Val Ile Gly Cys Gly Thr Ser	
370 375	380	
Tyr His Ala Ala Val Ala Thr Arg Gln Val	Leu Glu Glu Leu Thr Glu	
385 390	395	400
Leu Pro Val Met Val Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr		
405	410	415
Pro Val Phe Arg Asp Asp Val Cys Phe Phe Ile Ser Gln Ser Gly Glu		
420 425	430	
Thr Ala Asp Thr Leu Leu Ala Leu Arg Tyr Cys Lys Asp Arg Gly Ala		
435	440	445
Leu Thr Val Gly Val Thr Asn Thr Val Gly Ser Ser Ile Ser Arg Glu		
450 455	460	
Thr Asp Cys Gly Val His Ile Asn Ala Gly Pro Glu Val Gly Val Ala		
465 470	475	480
Ser Thr Lys Ala Tyr Thr Ser Gln Phe Ile Ser Leu Val Met Phe Gly		
485	490	495
Leu Met Met Ser Glu Asp Arg Ile Ser Leu Gln Asn Arg Arg Gln Glu		
500	505	510
Ile Ile Arg Gly Leu Arg Ser Leu Pro Glu Leu Ile Lys Glu Val Leu		
515	520	525
Ser Leu Glu Glu Lys Ile His Asp Leu Ala Leu Glu Leu Tyr Thr Gln		
530 535	540	
Arg Ser Leu Leu Val Met Gly Arg Gly Tyr Asn Tyr Ala Thr Cys Leu		
545 550	555	560
Glu Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly		
565	570	575
Ile Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp Lys		
580	585	590
Gln Met Pro Val Ile Met Val Ile Met Lys Asp Pro Cys Phe Ala Lys		
595	600	605
Cys Gln Asn Ala Leu Gln Gln Val Thr Ala Arg Gln Gly Arg Pro Ile		
610	615	620
Ile Leu Cys Ser Lys Asp Asp Thr Glu Ser Ser Lys Phe Ala Tyr Lys		
625 630	635	640
Thr Ile Glu Leu Pro His Thr Val Asp Cys Leu Gln Gly Ile Leu Ser		
645	650	655
Val Ile Pro Leu Gln Leu Leu Ser Phe His Leu Ala Val Leu Arg Gly		
660	665	670
Tyr Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu		
675	680	685

GFAT-anglais

<210> 11  
 <211> 2118  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> modified GFAT1Alt by an internal purification tag

<220>  
 <221> CDS  
 <222> (1)..(2118)  
 <223>

<220>  
 <221> misc\_feature  
 <222> (170)..(170)  
 <223> t or c

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Met Cys Gly Ile Phe Ala Tyr Leu Asn Tyr His Val Pro Arg Thr Arg		
1 5 10 15		
cga gaa atc ctg gag acc cta atc aaa ggc ctt cag aga ctg gag tac		96
Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr		
20 25 30		
aga gga tat gat tct gct ggt gtg gga ttt gat gga ggc aat gat aaa		144
Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys		
35 40 45		
gat tgg gaa gcc aat gcc tgc aaa anc cag ctt att aag aag aaa gga		192
Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly		
50 55 60		
aaa gtt aag gca ctg gat gaa gaa gtt cac aag caa caa gat atg gat		240
Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp		
65 70 75 80		
ttg gat ata gaa ttt gat gta cac ctt gga ata gct cat acc cgt tgg		288
Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp		
85 90 95		
gca aca cat gga gaa ccc agt cct gtc aat agc cac ccc cag cgc tct		336
Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser		
100 105 110		
gat aaa aat aat gaa ttt atc gtt att cac aat gga atc atc acc aac		384
Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn		
115 120 125		
tac aaa gac ttg aaa aag ttt ttg gaa agc aaa ggc tat gac ttc gaa		432
Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu		
130 135 140		
tct gaa aca gac aca gag aca att gcc aag ctc gtt aag tat atg tat		480
Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr		
145 150 155 160		
gac aat cgg gaa agt caa gat acc agc ttt act acc ttg gtg gag aga		528

GFAT-anglais															
Asp	Asn	Arg	Glu	Ser	Gln	Asp	Thr	Ser	Phe	Thr	Thr	Leu	Val	Glu	Arg
165									170						175
gtt	atc	caa	caa	ttg	gaa	ggt	gct	ttt	gca	ctt	gtg	ttt	aaa	agt	gtt
Val	Ile	Gln	Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val
180								185							190
cat	ttt	ccc	ggg	caa	gca	gtt	ggc	aca	agg	cga	ggt	agc	cct	ctg	ttg
His	Phe	Pro	Gly	Gln	Ala	Val	Gly	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu
195							200					205			
att	ggt	gta	cgg	agt	gaa	cat	aaa	ctt	tct	act	gat	cac	att	cct	ata
Ile	Gly	Val	Arg	Ser	Glu	His	Lys	Leu	Ser	Thr	Asp	His	Ile	Pro	Ile
210						215					220				
ctc	tac	aga	aca	gct	agg	act	cag	att	gga	tca	aaa	ttc	aca	cgg	ttg
Leu	Tyr	Arg	Thr	Ala	Arg	Thr	Gln	Ile	Gly	Ser	Lys	Phe	Thr	Arg	Trp
									235						
225							230								240
gga	tca	cag	gga	gaa	aga	ggc	aaa	gac	aag	aaa	gga	agc	tgc	aat	ctc
Gly	Ser	Gln	Gly	Glu	Arg	Gly	Lys	Asp	Lys	Lys	Gly	Ser	Cys	Asn	Leu
									250						
245															255
tct	cgt	gtg	gac	agc	aca	acc	tgc	ctt	ttc	ccg	gtg	gaa	gaa	aaa	gca
Ser	Arg	Val	Asp	Ser	Thr	Thr	Cys	Leu	Phe	Pro	Val	Glu	Glu	Lys	Ala
									265						
260												270			
gtg	gag	tat	taC	ttt	gct	tct	gat	gca	agt	gct	gtc	ata	gaa	cac	acc
Val	Glü	Tyr	Tyr	Phe	Ala	Ser	Asp	Ala	Ser	Ala	Val	Ile	Glü	His	Thr
									280						
275												285			
aat	cgc	gtc	atc	ttt	ctg	gaa	gat	gat	gat	gtt	gca	gca	gta	gtg	gat
Asn	Arg	Val	Ile	Phe	Leu	Glu	Asp	Asp	Asp	Val	Ala	Ala	Ala	Val	Asp
									295						
290												300			
gga	cgt	ctt	tct	atc	cat	cga	att	aaa	cga	act	gca	gga	cat	cac	cat
Gly	Arg	Leu	Ser	Ile	His	Arg	Ile	Lys	Arg	Thr	Ala	Gly	His	His	His
									310						
305												315			320
cac	cat	cac	gat	cac	ccc	gga	cga	gct	gtg	caa	aca	ctc	cag	atg	gaa
His	His	His	Asp	His	Pro	Gly	Arg	Ala	Val	Gln	Thr	Leu	Gln	Met	Glü
									325						
												330			
ctc	cag	cag	atc	atg	aag	ggc	aac	ttc	agt	tca	ttt	atg	cag	aag	gaa
Leu	Gln	Gln	Ile	Met	Lys	Gly	Asn	Phe	Ser	Ser	Phe	Met	Gln	Lys	Glü
									340				350		
345															
ata	ttt	gag	cag	cca	gag	tct	gtc	gtg	aac	aca	atg	aga	gga	aga	gtc
Ile	Phe	Glu	Gln	Pro	Glu	Ser	Val	Val	Asn	Thr	Met	Arg	Gly	Arg	Val
									355				365		
360															
aac	ttt	gat	gac	tat	act	gtg	aat	ttg	ggt	ggt	ttg	aag	gat	cac	ata
Asn	Phe	Asp	Asp	Tyr	Thr	Val	Asn	Leu	Gly	Gly	Leu	Lys	Asp	His	Ile
									370						
												375			
385															
aag	gag	atc	cag	aga	tgc	cgg	cgt	ttg	att	ctt	att	gct	tgt	gga	aca
Lys	Glu	Ile	Gln	Arg	Cys	Arg	Arg	Leu	Ile	Leu	Ile	Ala	Cys	Gly	Thr
									390				395		
															400
405															
agt	tac	cat	gct	ggt	gta	gca	aca	cgt	caa	gtt	ctt	gag	gag	ctg	act
Ser	Tyr	His	Ala	Gly	Val	Ala	Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr
									410						
															415

GFAT-anglais																	
gag	ttg	cct	gtg	atg	gtg	gaa	cta	gca	agt	gac	ttc	ctg	gac	aga	aac		1296
Glu	Leu	Pro	Val	Met	Val	Glu	Leu	Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn		
420						425						430					
aca	cca	gtc	ttt	cga	gat	gat	gtt	tgc	ttt	ttc	ctt	agt	caa	tca	ggt		1344
Thr	Pro	Val	Phe	Arg	Asp	Asp	Val	Cys	Phe	Phe	Leu	Ser	Gln	Ser	Gly		
435					440						445						
gag	aca	gca	gat	act	ttg	atg	ggt	ctt	cgt	tac	tgt	aag	gag	aga	gga		1392
Glu	Thr	Ala	Asp	Thr	Leu	Met	Gly	Leu	Arg	Tyr	Cys	Lys	Gl	Arg	Gly		
450					455					460							
gct	tta	act	gtg	ggg	atc	aca	aac	aca	gtt	ggc	agt	tcc	ata	tca	cgg		1440
Ala	Leu	Thr	Val	Gly	Ile	Thr	Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg		
465					470					475					480		
gag	aca	gat	tgt	gga	gtt	cat	att	aat	gct	ggt	cct	gag	att	ggt	gtg		1488
Glu	Thr	Asp	Cys	Gly	Val	His	Ile	Asn	Ala	Gly	Pro	Glu	Ile	Gly	Val		
485						490							495				
gcc	agt	aca	aag	gct	tat	acc	agc	cag	ttt	gta	tcc	ctt	gtg	atg	ttt		1536
Ala	Ser	Thr	Lys	Ala	Tyr	Thr	Ser	Gln	Phe	Val	Ser	Leu	Val	Met	Phe		
500						505						510					
gcc	ctt	atg	atg	tgt	gat	gat	cg	atc	tcc	atg	caa	gaa	aga	cgc	aaa		1584
Ala	Leu	Met	Met	Cys	Asp	Asp	Arg	Ile	Ser	Met	Gln	Glu	Arg	Arg	Lys		
515					520						525						
gag	atc	atg	ctt	gga	ttg	aaa	cg	ctg	cct	gat	ttg	att	aag	gaa	gta		1632
Glu	Ile	Met	Leu	Gly	Leu	Lys	Arg	Leu	Pro	Asp	Leu	Ile	Lys	Glu	Val		
530					535						540						
ctg	agc	atg	gat	gac	gaa	att	cag	aaa	cta	gca	aca	gaa	ctt	tat	cat		1680
Leu	Ser	Met	Asp	Asp	Glu	Ile	Gln	Lys	Leu	Ala	Thr	Glu	Leu	Tyr	His		
545					550					555				560			
cag	aag	tca	gtt	ctg	ata	atg	gga	cga	g	tat	cat	tat	gct	act	tgt		1728
Gln	Lys	Ser	Val	Leu	Ile	Met	Gly	Arg	Gly	Tyr	His	Tyr	Ala	Thr	Cys		
565						570						575					
ctt	gaa	ggg	gca	ctg	aaa	atc	aaa	gaa	att	act	tat	atg	cac	tct	gaa		1776
Leu	Glu	Gly	Ala	Leu	Lys	Ile	Lys	Glu	Ile	Thr	Tyr	Met	His	Ser	Glu		
580						585						590					
ggc	atc	ctt	gct	ggt	gaa	ttg	aaa	cat	ggc	cct	ctg	gct	ttg	gtg	gat		1824
Gly	Ile	Leu	Ala	Gly	Glu	Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Val	Asp		
595					600						605						
aaa	ttg	atg	cct	gtg	atc	atg	atc	atc	atg	aga	gat	cac	act	tat	gcc		1872
Lys	Leu	Met	Pro	Val	Ile	Met	Ile	Ile	Met	Arg	Asp	His	Thr	Tyr	Ala		
610					615					620							
aag	tgt	cag	aat	gct	ctt	cag	caa	gtg	gtt	gct	cg	cag	ggg	cg	cct		1920
Lys	Cys	Gln	Asn	Ala	Leu	Gln	Gln	Val	Val	Ala	Arg	Gln	Gly	Arg	Pro		
625					630					635				640			
gtg	gta	att	tgt	gat	aag	gag	gat	act	gag	acc	att	aag	aac	aca	aaa		1968
Val	Val	Ile	Cys	Asp	Lys	Glu	Asp	Thr	Glu	Thr	Ile	Lys	Asn	Thr	Lys		
645						650					655						
aga	acg	atc	aag	gtg	ccc	cac	tca	gtg	gac	tgc	ttg	cag	ggc	att	ctc		2016
Arg	Thr	Ile	Lys	Val	Pro	His	Ser	Val	Asp	Cys	Leu	Gln	Gly	Ile	Leu		

	<b>GFAT-anglais</b>		
660	665	670	
agc gtg atc cct tta cag ttg ctg gct ttc cac ctt gct gtg ctg aga Ser Val Ile Pro Leu Gln Leu Leu Ala Phe His Leu Ala Val Leu Arg			2064
675	680	685	
ggc tat gat gtt gat ttc cca cgg aat ctt gcc aaa tct gtg act gta Gly Tyr Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val			2112
690	695	700	
gag tga Glu 705			2118
<p>&lt;210&gt; 12</p> <p>&lt;211&gt; 705</p> <p>&lt;212&gt; PRT</p> <p>&lt;213&gt; Artificial sequence</p> <p>&lt;220&gt;</p> <p>&lt;221&gt; misc_feature</p> <p>&lt;222&gt; (57) : .(57)</p> <p>&lt;223&gt; 'xaa' in position 57 represents Thr or Ile</p> <p>&lt;220&gt;</p> <p>&lt;223&gt; modified GFAT1Alt by an internal purification tag</p> <p>&lt;400&gt; 12</p>			
Met Cys Gly Ile Phe Ala Tyr Leu Asn Tyr His Val Pro Arg Thr Arg 1 5 10 15			
Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr 20 25 30			
Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys 35 40 45			
Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly 50 55 60			
Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp 65 70 75 80			
Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp 85 90 95			
Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser 100 105 110			
Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn 115 120 125			
Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu 130 135 140			
Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr 145 150 155 160			
Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg 165 170 175			
Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val			

GFAT-anglais

180	185	190
His Phe Pro Gly Gln Ala Val	Gly Thr Arg Arg Gly Ser	Pro Leu Leu
195 196 197 198 199 200	200 201 202 203 204 205	205
Ile Gly Val Arg Ser Glu His	Lys Leu Ser Thr Asp His	Ile Pro Ile
210 211 212 213 214 215	215 216 217 218 219 220	220
Leu Tyr Arg Thr Ala Arg	Thr Gln Ile Gly Ser	Lys Phe Thr Arg Trp
225 226 227 228 229 230	230 231 232 233 234 235	235 240
Gly Ser Gln Gly Glu Arg Gly	Lys Asp Lys Lys Gly Ser Cys	Asn Leu
245 246 247 248 249 250	250 251 252 253 254 255	255
Ser Arg Val Asp Ser Thr Thr	Cys Leu Phe Pro Val	Glu Glu Lys Ala
260 261 262 263 264 265	265 266 267 268 269 270	270
Val Glu Tyr Tyr Phe Ala Ser	Asp Ala Ser Ala Val	Ile Glu His Thr
275 276 277 278 279 280	280 281 282 283 284 285	285
Asn Arg Val Ile Phe Leu	Glu Asp Asp Asp Val	Ala Ala Val Val Asp
290 291 292 293 294 295	295 296 297 298 299 300	300
Gly Arg Leu Ser Ile His	Arg Ile Lys Arg Thr	Ala Gly His His His
305 306 307 308 309 310	310 311 312 313 314 315	315 320
His His His Asp His	Pro Gly Arg Ala Val	Gln Thr Leu Gln Met Glu
325 326 327 328 329 330	330 331 332 333 334 335	335
Leu Gln Gln Ile Met Lys	Gly Asn Phe Ser Ser Phe Met	Gln Lys Glu
340 341 342 343 344 345	345 346 347 348 349 350	350
Ile Phe Glu Gln Pro Glu Ser	Val Val Asn Thr Met Arg	Gly Arg Val
355 356 357 358 359 360	360 361 362 363 364 365	365
Asn Phe Asp Asp Tyr Thr	Val Asn Leu Gly Gly	Leu Lys Asp His Ile
370 371 372 373 374 375	375 376 377 378 379 380	380
Lys Glu Ile Gln Arg Cys	Arg Arg Leu Ile Leu	Ile Ala Cys Gly Thr
385 386 387 388 389 390	390 391 392 393 394 395	395 400
Ser Tyr His Ala Gly Val	Ala Thr Arg Gln Val	Leu Glu Glu Leu Thr
405 406 407 408 409 410	410 411 412 413 414 415	415
Glu Leu Pro Val Met Val	Glu Leu Ala Ser Asp Phe	Leu Asp Arg Asn
420 421 422 423 424 425	425 426 427 428 429 430	430
Thr Pro Val Phe Arg Asp	Asp Val Cys Phe Phe	Leu Ser Gln Ser Gly
435 436 437 438 439 440	440 441 442 443 444 445	445
Glu Thr Ala Asp Thr Leu	Met Gly Leu Arg Tyr	Cys Lys Glu Arg Gly
450 451 452 453 454 455	455 456 457 458 459 460	460
Ala Leu Thr Val Gly	Ile Thr Asn Thr Val	Gly Ser Ser Ile Ser Arg
465 466 467 468 469 470	470 471 472 473 474 475	475 480
Glu Thr Asp Cys Gly Val	His Ile Asn Ala Gly	Pro Glu Ile Gly Val
485 486 487 488 489 490	490 491 492 493 494 495	495
Ala Ser Thr Lys Ala Tyr	Thr Ser Gln Phe Val	Ser Leu Val Met Phe
500 501 502 503 504 505	505 506 507 508 509 510	510
Ala Leu Met Met Cys Asp	Asp Arg Ile Ser Met	Gln Glu Arg Arg Lys

		<b>GFAT-anglais</b>
515	520	525
Glu Ile Met Leu Gly Leu Lys Arg Leu Pro Asp	530	535
Leu Ile Lys Glu Val	540	
Leu Ser Met Asp Asp Glu Ile Gln Lys Leu Ala Thr Glu Leu Tyr His	545	550
555		560
Gln Lys Ser Val Leu Ile Met Gly Arg Gly Tyr His Tyr Ala Thr Cys	565	570
575		
Leu Glu Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu	580	585
590		
Gly Ile Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Val Asp	595	600
605		
Lys Leu Met Pro Val Ile Met Ile Ile Met Arg Asp His Thr Tyr Ala	610	615
620		
Lys Cys Gln Asn Ala Leu Gln Gln Val Val Ala Arg Gln Gly Arg Pro	625	630
635		640
Val Val Ile Cys Asp Lys Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys	645	650
655		
Arg Thr Ile Lys Val Pro His Ser Val Asp Cys Leu Gln Gly Ile Leu	660	665
670		
Ser Val Ile Pro Leu Gln Leu Leu Ala Phe His Leu Ala Val Leu Arg	675	680
685		
Gly Tyr Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val	690	695
700		
Glu		
705		

<210> 13  
 <211> 608  
 <212> PRT  
 <213> *Escherichia coli*

<400> 13																
Cys	Gly	Ile	Val	Gly	Ala	Ile	Ala	Gln	Arg	Asp	Val	Ala	Glu	Ile	Leu	
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Leu	Glu	Gly	Leu	Arg	Arg	Leu	Glu	Tyr	Arg	Gly	Tyr	Asp	Ser	Ala	Gly	
20					25							30				
Leu	Ala	Val	Val	Asp	Ala	Glu	Gly	His	Met	Thr	Arg	Leu	Arg	Arg	Leu	
35					40							45				
Gly	Lys	Val	Gln	Met	Leu	Ala	Gln	Ala	Ala	Glu	Glu	His	Pro	Leu	His	
50					55					60						
Gly	Gly	Thr	Gly	Ile	Ala	His	Thr	Arg	Trp	Ala	Thr	His	Gly	Glu	Pro	
65					70				75			80				
Ser	Glu	Val	Asn	Ala	His	Pro	His	Val	Ser	Glu	His	Ile	Val	Val	Val	
85					90							95				

GFAT-anglais

His	Asn	Gly	Ile	Ile	Glu	Asn	His	Glu	Pro	Leu	Arg	Glu	Glu	Leu	Lys	
100					105									110		
Ala	Arg	Gly	Tyr	Thr	Phe	Val	Ser	Glu	Thr	Asp	Thr	Glu	Val	Ile	Ala	
115					120									125		
His	Leu	Val	Asn	Trp	Glu	Leu	Lys	Gln	Gly	Gly	Thr	Leu	Arg	Glu	Ala	
130					135									140		
Val	Leu	Arg	Ala	Ile	Pro	Gln	Leu	Arg	Gly	Ala	Tyr	Gly	Thr	Val	Ile	
145					150									160		
Met	Asp	Ser	Arg	His	Pro	Asp	Thr	Leu	Leu	Ala	Ala	Arg	Ser	Gly	Ser	
165								170						175		
Pro	Leu	Val	Ile	Gly	Leu	Gly	Met	Gly	Glu	Asn	Phe	Ile	Ala	Ser	Asp	
180							185							190		
Gln	Leu	Ala	Leu	Leu	Pro	Val	Thr	Arg	Arg	Phe	Ile	Phe	Leu	Glu	Glu	
195							200							205		
Gly	Asp	Ile	Ala	Glu	Ile	Thr	Arg	Arg	Ser	Val	Asn	Ile	Phe	Asp	Lys	
210						215								220		
Thr	Gly	Ala	Glu	Val	Lys	Arg	Gln	Asp	Ile	Glu	Ser	Asn	Leu	Gln	Tyr	
225						230								235	240	
Asp	Ala	Gly	Asp	Lys	Gly	Ile	Tyr	Arg	His	Tyr	Met	Gln	Lys	Glu	Ile	
245							250							255		
Tyr	Glu	Gln	Pro	Asn	Ala	Ile	Lys	Asn	Thr	Leu	Thr	Gly	Arg	Ile	Ser	
260							265							270		
His	Gly	Gln	Val	Asp	Leu	Ser	Glu	Leu	Gly	Pro	Asn	Ala	Asp	Glu	Leu	
275							280							285		
Leu	Ser	Lys	Val	Glu	His	Ile	Gln	Ile	Leu	Ala	Cys	Gly	Thr	Ser	Tyr	
290							295							300		
Asn	Ser	Gly	Met	Val	Ser	Arg	Tyr	Trp	Phe	Glu	Ser	Leu	Ala	Gly	Ile	
305						310								315	320	
Pro	Cys	Asp	Val	Glu	Ile	Ala	Ser	Glu	Phe	Arg	Tyr	Arg	Lys	Ser	Ala	
325							330							335		
Val	Arg	Arg	Asn	Ser	Leu	Met	Ile	Thr	Leu	Ser	Gln	Ser	Gly	Glu	Thr	
340							345							350		
Ala	Asp	Thr	Leu	Ala	Gly	Leu	Arg	Leu	Ser	Lys	Glu	Leu	Gly	Tyr	Leu	
355							360							365		
Gly	Ser	Leu	Ala	Ile	Cys	Asn	Val	Pro	Gly	Ser	Ser	Leu	Val	Arg	Glu	
370							375							380		
Ser	Asp	Leu	Ala	Leu	Met	Thr	Asn	Ala	Gly	Thr	Glu	Ile	Gly	Val	Ala	
385							390							395	400	
Ser	Thr	Lys	Ala	Phe	Thr	Thr	Gln	Leu	Thr	Val	Leu	Leu	Met	Leu	Val	
405							410							415		
Ala	Lys	Leu	Ser	Arg	Leu	Lys	Gly	Leu	Asp	Ala	Ser	Ile	Glu	His	Asp	
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Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met Leu  
435 440 445 GFAT-anglais

Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp Lys  
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His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala Leu  
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Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu Ala  
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Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp Ala  
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Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu Lys  
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Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu Tyr  
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Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met His  
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Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe Tyr  
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Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys Gly  
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GFAT-anglais

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